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ggt ttt gtg ggc aac atg ctg gtc atc ctc atc ctg ata aac tgc caa Gly Phe Val Gly Asn Met Leu Val Ile Leu Ile Leu Ile Asn Cys Gln 45 50 55	435
agg ctg gag agc atg act gac atc tac ctg ctc aac ctg gcc atc tct Arg Leu Glu Ser Met Thr Asp Ile Tyr Leu Leu Asn Leu Ala Ile Ser 60 65 70 75	483
gac ctg ttt ttc ctt ctt act gtc ccc ttc tgg gct cac tat gct gcc Asp Leu Phe Phe Leu Leu Thr Val Pro Phe Trp Ala His Tyr Ala Ala 80 85 90	531
gcc cag tgg gac ttt gga aat aca atg tgt caa ctc ttg aca ggg ctc Ala Gln Trp Asp Phe Gly Asn Thr Met Cys Gln Leu Leu Thr Gly Leu 95 100 105	579
tat ttt ata ggc ttc ttc tct gga atc ttc ttc atc atc ctc ctg aca Tyr Phe Ile Gly Phe Phe Ser Gly Ile Phe Phe Ile Ile Leu Leu Thr 110 115 120	627
atc gat agg tac ctg gct atc gtc cat gct gtg ttt gct tta aaa gcc Ile Asp Arg Tyr Leu Ala Ile Val His Ala Val Phe Ala Leu Lys Ala 125 130 135	675
agg acg gtc acc ttt ggg gtg gtg aca agt gtg atc act tgg gtg gtg Arg Thr Val Thr Phe Gly Val Val Thr Ser Val Ile Thr Trp Val Val 140 145 150 155	723
gct gtg ttt gcg tct ctc cca gga atc atc ttt acc aga tct caa aaa Ala Val Phe Ala Ser Leu Pro Gly Ile Ile Phe Thr Arg Ser Gln Lys 160 165 170	771
gaa ggt ctt cat tac acc tgc agc tct cat ttt cca tac agt cag tat Glu Gly Leu His Tyr Thr Cys Ser Ser His Phe Pro Tyr Ser Gln Tyr 175 180 185	819
caa ttc tgg aag aat ttc cag aca tta aag ata gtc atc ttg ggg ctg Gln Phe Trp Lys Asn Phe Gln Thr Leu Lys Ile Val Ile Leu Gly Leu 190 195 200	867
gtc ctg ccg ctg ctt gtc atg gtc atc tgc tac tcg gga atc cta aaa Val Leu Pro Leu Leu Val Met Val Ile Cys Tyr Ser Gly Ile Leu Lys 205 210 215	915
act ctg ctt ccg tgt cga aat gag aag aag agg cac agg gct gtg agg Thr Leu Leu Arg Cys Arg Asn Glu Lys Lys Arg His Arg Ala Val Arg 220 225 230 235	963
ctt atc ttc acc atc atg att gtt tat ttt ctc ttc tgg gct ccc tac Leu Ile Phe Thr Ile Met Ile Val Tyr Phe Leu Phe Trp Ala Pro Tyr 240 245 250	1011
aac att gtc ctt ctc ctg aac acc ttc cag gaa ttc ttt ggc ctg aat Asn Ile Val Leu Leu Leu Asn Thr Phe Gln Glu Phe Phe Gly Leu Asn 255 260 265	1059
aat tgc agt agc tct aac agg ttg gac caa gct atg cag gtg aca gag Asn Cys Ser Ser Ser Asn Arg Leu Asp Gln Ala Met Gln Val Thr Glu 270 275 280	1107

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act ctt ggg atg acg cac tgc tgc atc aac ccc atc atc tat gcc ttt 1155
Thr Leu Gly Met Thr His Cys Cys Ile Asn Pro Ile Ile Tyr Ala Phe
285 290 295

gtc ggg gag aag ttc aga aac tac ctc tta gtc ttc ttc caa aag cac 1203
Val Gly Glu Lys Phe Arg Asn Tyr Leu Leu Val Phe Phe Gln Lys His
300 305 310 315

att gcc aaa cgc ttc tgc aaa tgc tgt tct att ttc cag caa gag gct 1251
Ile Ala Lys Arg Phe Cys Lys Cys Cys Ser Ile Phe Gln Gln Glu Ala
320 325 330

ccc gag cga gca agc tca gtt tac acc cga tcc act ggg gag cag gaa 1299
Pro Glu Arg Ala Ser Ser Val Tyr Thr Arg Ser Thr Gly Glu Gln Glu
335 340 345

ata tct gtg ggc ttg tgacacggac tcaagtgggc tgggtgaccca gtcagagttg 1354
Ile Ser Val Gly Leu
350

tgacacatggc ttagtttttca tacacagcct gggctggggg tgggggtggaa gaggtctttt 1414

<210> 2
<211> 352
<212> PRT
<213> Homo sapiens

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Ser Glu Pro Cys Pro Lys Ile Asn Val Lys Gln Ile Ala Ala Arg Leu
20 25 30
Leu Pro Pro Leu Tyr Ser Leu Val Phe Ile Phe Gly Phe Val Gly Asn
35 40 45
Met Leu Val Ile Leu Ile Leu Ile Asn Cys Gln Arg Leu Glu Ser Met
50 55 60
Thr Asp Ile Tyr Leu Leu Asn Leu Ala Ile Ser Asp Leu Phe Phe Leu
65 70 75 80
Leu Thr Val Pro Phe Trp Ala His Tyr Ala Ala Ala Gln Trp Asp Phe
85 90 95
Gly Asn Thr Met Cys Gln Leu Leu Thr Gly Leu Tyr Phe Ile Gly Phe
100 105 110
Phe Ser Gly Ile Phe Phe Ile Ile Leu Leu Thr Ile Asp Arg Tyr Leu
115 120 125
Ala Ile Val His Ala Val Phe Ala Leu Lys Ala Arg Thr Val Thr Phe
130 135 140
Gly Val Val Thr Ser Val Ile Thr Trp Val Val Ala Val Phe Ala Ser
145 150 155 160
Leu Pro Gly Ile Ile Phe Thr Arg Ser Gln Lys Glu Gly Leu His Tyr
165 170 175

100570002900

Thr Cys Ser Ser His Phe Pro Tyr Ser Gln Tyr Gln Phe Trp Lys Asn
180 185 190

Phe Gln Thr Leu Lys Ile Val Ile Leu Gly Leu Val Leu Pro Leu Leu
195 200 205

Val Met Val Ile Cys Tyr Ser Gly Ile Leu Lys Thr Leu Leu Arg Cys
210 215 220

Arg Asn Glu Lys Lys Arg His Arg Ala Val Arg Leu Ile Phe Thr Ile
225 230 235 240

Met Ile Val Tyr Phe Leu Phe Trp Ala Pro Tyr Asn Ile Val Leu Leu
245 250 255

Leu Asn Thr Phe Gln Glu Phe Phe Gly Leu Asn Asn Cys Ser Ser Ser
260 265 270

Asn Arg Leu Asp Gln Ala Met Gln Val Thr Glu Thr Leu Gly Met Thr
275 280 285

His Cys Cys Ile Asn Pro Ile Ile Tyr Ala Phe Val Gly Glu Lys Phe
290 295 300

Arg Asn Tyr Leu Leu Val Phe Phe Gln Lys His Ile Ala Lys Arg Phe
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Cys Lys Cys Cys Ser Ile Phe Gln Gln Glu Ala Pro Glu Arg Ala Ser
325 330 335

Ser Val Tyr Thr Arg Ser Thr Gly Glu Gln Glu Ile Ser Val Gly Leu
340 345 350

<210> 3
<211> 30
<212> DNA
<213> Artificial

<220>
<223> 5' Oligonucleotide primer for HDGNR10

<400> 3
cggaattcct ccatggatta tcaagtgtca

30

<210> 4
<211> 29
<212> DNA
<213> Artificial

<220>
<223> 3' Oligonucleotide primer for HDGNR10

<400> 4
cggaagcttc gtcacaagcc cacagatat

29

<210> 5
<211> 34
<212> DNA

Ile Leu Ile Asn Cys Lys Lys Leu Lys Cys Leu Thr Asp Ile Tyr Leu
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Leu Asn Leu Ala Ile Ser Asp Leu Leu Phe Leu Ile Thr Leu Pro Leu
 65 70 75 80
 Trp Ala His Ser Ala Ala Asn Glu Trp Val Phe Gly Asn Ala Met Cys
 85 90 95
 Lys Leu Phe Thr Gly Leu Tyr His Ile Gly Tyr Phe Gly Gly Ile Phe
 100 105 110
 Phe Ile Ile Leu Leu Thr Ile Asp Arg Tyr Leu Ala Ile Val His Ala
 115 120 125
 Val Phe Ala Leu Lys Ala Arg Thr Val Thr Phe Gly Val Val Thr Ser
 130 135 140
 Val Ile Thr Trp Leu Val Ala Val Phe Ala Ser Val Pro Gly Ile Ile
 145 150 155 160
 Phe Thr Lys Cys Gln Lys Glu Asp Ser Val Tyr Val Cys Gly Pro Tyr
 165 170 175
 Phe Pro Arg Gly Trp Asn Asn Phe His Thr Ile Met Arg Asn Ile Leu
 180 185 190
 Gly Leu Val Leu Pro Leu Leu Ile Met Val Ile Cys Tyr Ser Gly Ile
 195 200 205
 Leu Lys Thr Leu Leu Arg Cys Arg Asn Glu Lys Lys Arg His Arg Ala
 210 215 220
 Val Arg Val Ile Phe Thr Ile Met Ile Val Tyr Phe Leu Phe Trp Thr
 225 230 235 240
 Pro Tyr Asn Ile Val Ile Leu Leu Asn Thr Phe Gln Glu Phe Phe Gly
 245 250 255
 Leu Ser Asn Cys Glu Ser Thr Ser Gln Leu Asp Gln Ala Thr Gln Val
 260 265 270
 Thr Glu Thr Leu Gly Met Thr His Cys Cys Ile Asn Pro Ile Ile Tyr
 275 280 285
 Ala Phe Val Gly Glu Lys Phe Arg Ser Leu Phe His Ile Ala Leu Gly
 290 295 300
 Cys Arg Ile Ala Pro Leu Gln Lys Pro Val Cys Gly Gly Pro Gly Val
 305 310 315 320
 Arg Pro Gly Lys Asn Val Lys Val Thr Thr Gln Gly Leu Leu Asp Gly
 325 330 335
 Arg Gly Lys Gly Lys Ser Ile Gly
 340

<210> 10
 <211> 733
 <212> DNA
 <213> Homo sapiens

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 aattcgaggg tgcaccgtca gtcttctct tcccccaaa acccaaggac accctcatga 120

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tctcccgga ccttgaggtc acatgogtgg tgggtggacgt aagccacgaa gaccctgagg 180
tcaagttcaa ctggtacgtg gacggcggtg aggtgcataa tgccaagaca aagccgcggg 240
aggagcagta caacagcacg tacctgtgtg tcagcgtcct caccgtcctg caccaggact 300
ggctgaatgg caaggagtac aagtgaagg tctccaacaa agccctccca acccccatcg 360
agaaaacccat ctcaaagcc aaagggcagc cccgagaacc acaggtgtac accctgcccc 420
catcccgga tgagctgacc aagaaccagg tcagcctgac ctgcctggtc aaaggcttct 480
atccaagcga catcgccgtg gagtgggaga gcaatgggca gccggagAAC aactacaaga 540
ccacgcctcc cgtgctggac tccgaaggct ccttcttct ctacagcaag ctcaccgtgg 600
acaagagcag gtggcagcag gggaacgtct tctcatgctc cgtgatgcat gaggtctctg 660
acaaccacta cagcagaag agcctctccc tgtctccggg taaatgagtg cgacggccgc 720
gactctagag gat 733
```

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<210> 11
<211> 5
<212> PRT
<213> Membrane proximal region motif
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<220>
<221> Variant
<222> (3)
<223> May be any amino acid
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<400> 11
Trp Ser Xaa Trp Ser
1 5
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```
<210> 12
<211> 86
<212> DNA
<213> Artificial
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<220>
<223> 5' Primer for Gamma Activation Site-SV40 Early Promoter Construct
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<400> 12
gcgcctcgag atttccccga aatctagatt tccccgaaat gatttccccg aaatgatttc 60
cccgaaatat ctgcatctc aattag 86
```

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<210> 13
<211> 27
<212> DNA
<213> Artificial
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<220>
<223> 3' Oligonucleotide primer for SV40 Early Promoter
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```
<400> 13
gcggcaagct ttttgcaaag cctaggc 27
```

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<210> 14
<211> 271
<212> DNA
<213> Artificial

<220>
<223> Gamma Activation Site-SV40 Early Promoter Construct

<400> 14
ctcgagattt ccccgaaatc tagattttccc cgaaatgatt tccccgaaat gatttccccg 60
aaatatctgc catctcaatt agtcagcaac catagtcccg cccctaactc cgcccatccc 120
gcccctaact ccgcccagtt ccgcccattc tccgcccatt ggctgactaa ttttttttat 180
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ttttggaggc ctaggctttt gcaaaaagct t 271

<210> 15
<211> 32
<212> DNA
<213> Artificial

<220>
<223> 5' Oligonucleotide primer for EGR-1 Promoter Sequence

<400> 15
gcgctcgagg gatgacagcg atagaacccc gg 32

<210> 16
<211> 31
<212> DNA
<213> Artificial

<220>
<223> 3' Oligonucleotide primer for EGR-1 Promoter Sequence

<400> 16
gcgaagcttc gcgactcccc ggatccgcct c 31

<210> 17
<211> 12
<212> DNA
<213> Homo Sapiens

<400> 17
ggggactttc cc 12

<210> 18
<211> 73
<212> DNA
<213> Artificial

<220>
<223> 5' Oligonucleotide primer for NF-KB-SV40 Early Promoter Construct

<400> 18
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73

```
<400> 19
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27

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<400> 20
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cagttccgcc cattctccgc cccatggctg actaattttt tttatttatg cagaggccga    180
ggccgcctcg gcctctgagc tattccagaa gtagtgagga ggcttttttg gaggcctagg    240
cttttgcaaa aagctt                                     256
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<221> CDS
<222> (1)..(1056)
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Met	Asp	Tyr	Gln	Val	Ser	Ser	Pro	Ile	Tyr	Asp	Ile	Asn	Tyr	Tyr	Thr	
1				5					10					15		
tcg	gag	ccc	tgc	caa	aaa	atc	aat	gtg	aag	caa	atc	gca	gcc	cgc	ctc	96
Ser	Glu	Pro	Cys	Gln	Lys	Ile	Asn	Val	Lys	Gln	Ile	Ala	Ala	Arg	Leu	
			20					25					30			
ctg	cct	ccg	ctc	tac	tca	ctg	gtg	ttc	atc	ttt	ggt	ttt	gtg	ggc	aac	144
Leu	Pro	Pro	Leu	Tyr	Ser	Leu	Val	Phe	Ile	Phe	Gly	Phe	Val	Gly	Asn	
		35					40					45				
atg	ctg	gtc	atc	ctc	atc	ctg	ata	aac	tgc	aaa	agg	ctg	aag	agc	atg	192
Met	Leu	Val	Ile	Leu	Ile	Leu	Ile	Asn	Cys	Lys	Arg	Leu	Lys	Ser	Met	
	50					55				60						
act	gac	atc	tac	ctg	ctc	aac	ctg	gcc	atc	tct	gac	ctg	ttt	ttc	ctt	240

Thr 65	Asp	Ile	Tyr	Leu 70	Leu	Asn	Leu	Ala	Ile	Ser 75	Asp	Leu	Phe	Phe	Leu 80	
ctt	act	gtc	ccc	ttc	tgg	gct	cac	tat	gct	gcc	gcc	cag	tgg	gac	ttt	288
Leu	Thr	Val	Pro	Phe 85	Trp	Ala	His	Tyr	Ala 90	Ala	Ala	Gln	Trp	Asp	Phe	
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Gly	Asn	Thr	Met	Cys 100	Gln	Leu	Leu	Thr 105	Gly	Leu	Tyr	Phe	Ile 110	Gly	Phe	
ttc	tct	gga	atc	ttc	ttc	atc	atc	ctc	ctg	aca	atc	gat	agg	tac	ctg	384
Phe	Ser	Gly	Ile	Phe 115	Phe	Ile	Ile	Leu 120	Leu	Thr	Ile	Asp 125	Arg	Tyr	Leu	
gct	gtc	gtc	cat	gct	gtg	ttt	gct	tta	aaa	gcc	agg	acg	gtc	acc	ttt	432
Ala	Val	Val	His	Ala 130	Val	Phe 135	Ala	Leu	Lys	Ala	Arg	Thr 140	Val	Thr	Phe	
ggg	gtg	gtg	aca	agt	gtg	atc	act	tgg	gtg	gtg	gct	gtg	ttt	gcg	tct	480
Gly	Val	Val	Thr	Ser 145	Val	Ile 150	Thr	Trp	Val	Val	Ala	Val 155	Phe	Ala	Ser 160	
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Leu	Pro	Gly	Ile	Ile 165	Phe	Thr	Arg	Ser 170	Gln	Lys	Glu	Gly	Leu	His 175	Tyr	
acc	tgc	agc	tct	cat	ttt	cca	tac	agt	cag	tat	caa	ttc	tgg	aag	aat	576
Thr	Cys	Ser	Ser	His 180	Phe	Pro	Tyr	Ser 185	Gln	Tyr	Gln	Phe	Trp 190	Lys	Asn	
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Phe	Gln	Thr	Leu	Lys 195	Ile	Val	Ile 200	Leu	Gly	Leu	Val	Leu 205	Pro	Leu	Leu	
gtc	atg	gtc	atc	tgc	tac	tgc	gga	atc	cta	aaa	act	ctg	ctt	cgg	tgt	672
Val	Met	Val	Ile	Cys 210	Tyr	Ser 215	Gly	Ile	Leu	Lys	Thr 220	Leu	Leu	Arg	Cys	
cga	aat	gag	aag	aag	agg	cac	agg	gct	gtg	agg	ctt	atc	ttc	acc	atc	720
Arg	Asn	Glu	Lys	Lys 225	Arg	His 230	Arg	Ala	Val	Arg 235	Leu	Ile	Phe	Thr 240	Ile	
atg	att	gtt	tat	ttt	ctc	ttc	tgg	gct	ccc	tac	aac	att	gtc	ctt	ctc	768
Met	Ile	Val	Tyr	Phe 245	Leu	Phe	Trp	Ala	Pro 250	Tyr	Asn	Ile	Val	Leu 255	Leu	
ctg	aac	acc	ttc	cag	gaa	ttc	ttt	ggc	ctg	aat	aat	tgc	agt	agc	tct	816
Leu	Asn	Thr	Phe 260	Gln	Glu	Phe	Phe 265	Gly	Leu	Asn	Asn	Cys	Ser 270	Ser	Ser	
aac	agg	ttg	gac	caa	gct	atg	cag	gtg	aca	gag	act	ctt	ggg	atg	acg	864
Asn	Arg	Leu	Asp	Gln 275	Ala	Met	Gln 280	Val	Thr	Glu	Thr 285	Leu	Gly	Met	Thr	
cac	tgc	tgc	atc	aac	ccc	atc	atc	tat	gcc	ttt	gtc	ggg	gag	aag	ttc	912
His	Cys	Cys	Ile	Asn 290	Pro	Ile 295	Ile	Tyr	Ala	Phe	Val 300	Gly	Glu	Lys	Phe	
aga	aac	tac	ctc	tta	gtc	ttc	ttc	caa	aag	cac	att	gcc	aaa	cgc	ttc	960
Arg	Asn	Tyr	Leu	Leu 305	Val 310	Phe	Phe	Gln	Lys	His 315	Ile	Ala	Lys	Arg	Phe 320	

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Cys Lys Cys Cys Ser Ile Phe Gln Gln Glu Ala Pro Glu Arg Ala Ser
325 330 335

tca gtt tac acc cga tcc act gag gag cag gaa ata tct gtg ggc ttg 1056
Ser Val Tyr Thr Arg Ser Thr Glu Glu Gln Glu Ile Ser Val Gly Leu
340 345 350

<210> 22
<211> 352
<212> PRT
<213> Homo sapiens

<400> 22
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1 5 10 15

Ser Glu Pro Cys Gln Lys Ile Asn Val Lys Gln Ile Ala Ala Arg Leu
20 25 30

Leu Pro Pro Leu Tyr Ser Leu Val Phe Ile Phe Gly Phe Val Gly Asn
35 40 45

Met Leu Val Ile Leu Ile Leu Ile Asn Cys Lys Arg Leu Lys Ser Met
50 55 60

Thr Asp Ile Tyr Leu Leu Asn Leu Ala Ile Ser Asp Leu Phe Phe Leu
65 70 75 80

Leu Thr Val Pro Phe Trp Ala His Tyr Ala Ala Ala Gln Trp Asp Phe
85 90 95

Gly Asn Thr Met Cys Gln Leu Leu Thr Gly Leu Tyr Phe Ile Gly Phe
100 105 110

Phe Ser Gly Ile Phe Phe Ile Ile Leu Leu Thr Ile Asp Arg Tyr Leu
115 120 125

Ala Val Val His Ala Val Phe Ala Leu Lys Ala Arg Thr Val Thr Phe
130 135 140

Gly Val Val Thr Ser Val Ile Thr Trp Val Val Ala Val Phe Ala Ser
145 150 155 160

Leu Pro Gly Ile Ile Phe Thr Arg Ser Gln Lys Glu Gly Leu His Tyr
165 170 175

Thr Cys Ser Ser His Phe Pro Tyr Ser Gln Tyr Gln Phe Trp Lys Asn
180 185 190

Phe Gln Thr Leu Lys Ile Val Ile Leu Gly Leu Val Leu Pro Leu Leu
195 200 205

Val Met Val Ile Cys Tyr Ser Gly Ile Leu Lys Thr Leu Leu Arg Cys
210 215 220

Arg Asn Glu Lys Lys Arg His Arg Ala Val Arg Leu Ile Phe Thr Ile
225 230 235 240

Met Ile Val Tyr Phe Leu Phe Trp Ala Pro Tyr Asn Ile Val Leu Leu
245 250 255

1005250-020000

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<210> 23
<211> 23
<212> DNA
<213> Artificial

<220>
<223> 5' Oligonucleotide primer for VH Domain

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caggtgcagc tgggtgcagtc tgg

<210> 24
<211> 23
<212> DNA
<213> Artificial

<220>
<223> 5' Oligonucleotide primer for VH Domain

<400> 24
caggtcaact taagggagtc tgg

<210> 25
<211> 23
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<400> 25
gaggtgcagc tgggtggagtc tgg

<210> 26
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23

24

<210> 32
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<212> DNA
<213> Artificial

<220>
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<400> 32
tgaggagacg gtgaccgtgg tccc

24

<210> 33
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<400> 33
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23

<210> 34
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<220>
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gatgttgtga tgactcagtc tcc

23

<210> 35
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<220>
<223> 5' Oligonucleotide primer for VL Domain

<400> 35
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23

<210> 36
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<212> DNA
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<220>
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<400> 36
gaaattgtgt tgacgcagtc tcc

23

<210> 37
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<223> 3' Oligonucleotide primer for VL Domain

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<213>	Artificial

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<212>	DNA
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```

<210>	50
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```
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acgtttgatc tccaccttgg tccc
```

```
<210> 51
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<212> DNA
<213> Artificial
```

<220>
<223> 3' Oligonucleotide primer for VL Domain

<400> 51
acgtttaatc tccagtcgtg tccc 24

<210>	52
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<212>	DNA
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<220>
<223> 3' Oligonucleotide primer for VL Domain

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<400> 52
cagtctgtgt tgacgcagcc gcc                                     23
```

<210> 53
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 <211> 23
 <212> DNA
 <213> Artificial
 <220>
 <223> 3' Oligonucleotide primer for VL Domain
 <400> 55
 tcttctgagc tgactcagga ccc 23
 <210> 56
 <211> 23
 <212> DNA
 <213> Artificial
 <220>
 <223> 3' Oligonucleotide primer for VL Domain
 <400> 56
 cacgttatac tgactcaacc gcc 23
 <210> 57
 <211> 23
 <212> DNA
 <213> Artificial
 <220>
 <223> 3' Oligonucleotide primer for VL Domain
 <400> 57
 caggctgtgc tcactcagcc gtc 23
 <210> 58
 <211> 23

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<212> DNA
<213> Artificial

<220>
<223> 3' Oligonucleotide primer for VL Domain

<400> 58
aattttatgc tgactcagcc cca 23

<210> 59
<211> 363
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (1)..(363)
<223>

<400> 59
cag gtg cag ctg cag gag tcg ggc cca gga ctg gtg aag cct tcg gag 48
Gln Val Gln Leu Gln Glu Ser Gly Pro Gly Leu Val Lys Pro Ser Glu
1 5 10 15

acc ctg tcc ctc acc tgc act gtc tct ggt ggc tcc atc agt agt ttc 96
Thr Leu Ser Leu Thr Cys Thr Val Ser Gly Gly Ser Ile Ser Ser Phe
20 25 30

tac tgg agc tgg atc cgg cag ccc gcc ggg aag gga ctg gac tgg att 144
Tyr Trp Ser Trp Ile Arg Gln Pro Ala Gly Lys Gly Leu Asp Trp Ile
35 40 45

ggg cgt atc tat acc agc ggg aac acc aac tac aac ccc tcc ctc aag 192
Gly Arg Ile Tyr Thr Ser Gly Asn Thr Asn Tyr Asn Pro Ser Leu Lys
50 55 60

agt cga gtc acc atg tca gta gac acg tcc aag aac cgg ttc tcc ctg 240
Ser Arg Val Thr Met Ser Val Asp Thr Ser Lys Asn Arg Phe Ser Leu
65 70 75 80

aaa ctg agc tct gtg acc gcc gcg gac acg gcc gtg tat tac tgt gcg 288
Lys Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr Cys Ala
85 90 95

aga gat cgg ggc agc agc tgg tac ccc gat gct ttt gat atc tgg ggc 336
Arg Asp Arg Gly Ser Ser Trp Tyr Pro Asp Ala Phe Asp Ile Trp Gly
100 105 110

caa ggg aca atg gtc acc gtc tcc tca 363
Gln Gly Thr Met Val Thr Val Ser Ser
115 120

<210> 60
<211> 121
<212> PRT
<213> Homo sapiens

<400> 60
Gln Val Gln Leu Gln Glu Ser Gly Pro Gly Leu Val Lys Pro Ser Glu
1 5 10 15

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Thr Leu Ser Leu Thr Cys Thr Val Ser Gly Gly Ser Ile Ser Ser Phe
 20 25 30
 Tyr Trp Ser Trp Ile Arg Gln Pro Ala Gly Lys Gly Leu Asp Trp Ile
 35 40 45
 Gly Arg Ile Tyr Thr Ser Gly Asn Thr Asn Tyr Asn Pro Ser Leu Lys
 50 55 60
 Ser Arg Val Thr Met Ser Val Asp Thr Ser Lys Asn Arg Phe Ser Leu
 65 70 75 80
 Lys Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr Cys Ala
 85 90 95
 Arg Asp Arg Gly Ser Ser Trp Tyr Pro Asp Ala Phe Asp Ile Trp Gly
 100 105 110
 Gln Gly Thr Met Val Thr Val Ser Ser
 115 120

<210> 61
 <211> 327
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (1)..(327)
 <223>

<400> 61
 gat att gtg ttg acg cat tct cca ggc acc ctg tct ttg tct cca ggg 48
 Asp Ile Val Leu Thr His Ser Pro Gly Thr Leu Ser Leu Ser Pro Gly
 1 5 10 15
 gaa aga gcc acc ctc tcc tgc agg gcc agt cag cgt gtt acc agc agc 96
 Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Arg Val Thr Ser Ser
 20 25 30
 tgc tta gcc tgg tac cag cag aaa cct ggc cag gct ccc agg ctc ctc 144
 Cys Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu
 35 40 45
 atc tat ggt aca tcc agc agg gcc act ggc atc cca gac agg ttc agt 192
 Ile Tyr Gly Thr Ser Ser Arg Ala Thr Gly Ile Pro Asp Arg Phe Ser
 50 55 60
 ggc agt ggg tct ggg aca gac ttc act ctc acc atc agc aga ctg gag 240
 Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Arg Leu Glu
 65 70 75 80
 cct gaa gat ttt gca gtg tat tac tgt cag cag tat gtt agc tca cct 288
 Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Tyr Val Ser Ser Pro
 85 90 95
 ctc acc ttc ggc caa ggg aca cga ctc gag atc aaa cgt 327
 Leu Thr Phe Gly Gln Gly Thr Arg Leu Glu Ile Lys Arg
 100 105

<210> 62

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<211> 109
<212> PRT
<213> Homo sapiens

<400> 62
Asp Ile Val Leu Thr His Ser Pro Gly Thr Leu Ser Leu Ser Pro Gly
1 5 10 15
Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Arg Val Thr Ser Ser
20 25 30
Cys Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu
35 40 45
Ile Tyr Gly Thr Ser Ser Arg Ala Thr Gly Ile Pro Asp Arg Phe Ser
50 55 60
Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Arg Leu Glu
65 70 75 80
Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Tyr Val Ser Ser Pro
85 90 95
Leu Thr Phe Gly Gln Gly Thr Arg Leu Glu Ile Lys Arg
100 105

<210> 63
<211> 379
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (1)..(378)
<223>

<400> 63
gag gtg cag ctg gtg gag tct ggg gga ggc ttg gta aag tct ggg ggg 48
Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Lys Ser Gly Gly
1 5 10 15
tcc ctt aga ctc tcc tgt gca gcc tcc gga ttc act ttc agt aac gcc 96
Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Asn Ala
20 25 30
tgg atg acc tgg gtc cgc cag gct cca ggg aag agg ctg gag tgg gtt 144
Trp Met Thr Trp Val Arg Gln Ala Pro Gly Lys Arg Leu Glu Trp Val
35 40 45
ggc cgt att aaa agc aat gct gat ggt ggg tca aca gac tac gct gca 192
Gly Arg Ile Lys Ser Asn Ala Asp Gly Gly Ser Thr Asp Tyr Ala Ala
50 55 60
ccc gtg aaa ggc aga ttc acc atc tca aga gat gat tca aaa aac acg 240
Pro Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asp Ser Lys Asn Thr
65 70 75 80
ctg tat ctg caa atg aac agc ctg aaa acc gag gac aca gcc gtg tat 288
Leu Tyr Leu Gln Met Asn Ser Leu Lys Thr Glu Asp Thr Ala Val Tyr
85 90 95
tac tgt aac aca gat aag ggt ggg agc tac ccc tac tac tac tac ggt 336

100575002500

cat gat gca tcc agt ttg caa agt ggg gtc cca tca agg ttc agc ggc 192

Tyr Asp Ala Ser Ser Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly
50 55 60

agt gga tct ggg aca gaa ttc act ctc aca atc agc agc ctg cag cct 240
Ser Gly Ser Gly Thr Glu Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65 70 75 80

gaa gat ttt gca act tat tac tgt cta cag cat aat agt tac cca ttc 288
Glu Asp Phe Ala Thr Tyr Tyr Cys Leu Gln His Asn Ser Tyr Pro Phe
85 90 95

act ttc ggc cct ggg acc aaa gtg gat atc aaa cga 324
Thr Phe Gly Pro Gly Thr Lys Val Asp Ile Lys Arg
100 105

<210> 66
<211> 108
<212> PRT
<213> Homo sapiens

<400> 66
Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
1 5 10 15

Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Gly Ile Arg Asn Asp
20 25 30

Leu Gly Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Arg Leu Ile
35 40 45

Tyr Asp Ala Ser Ser Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly
50 55 60

Ser Gly Ser Gly Thr Glu Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65 70 75 80

Glu Asp Phe Ala Thr Tyr Tyr Cys Leu Gln His Asn Ser Tyr Pro Phe
85 90 95

Thr Phe Gly Pro Gly Thr Lys Val Asp Ile Lys Arg
100 105

<210> 67
<211> 378
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (1)..(378)
<223>

<400> 67
gag gtg cag ctg gtg gag tct ggc cca gga ctg gtg aag cct tcg gag 48
Glu Val Gln Leu Val Glu Ser Gly Pro Gly Leu Val Lys Pro Ser Glu
1 5 10 15

acc ctg tcc ctc acc tgc act gtc tct ggt ggc tcc atc agt agt tac 96
Thr Leu Ser Leu Thr Cys Thr Val Ser Gly Gly Ser Ile Ser Ser Tyr
20 25 30

20057500.000000

tac tgg agc tgg atc cgg cag ccc cca ggg aag gga ctg gag tgg att 144
Tyr Trp Ser Trp Ile Arg Gln Pro Pro Gly Lys Gly Leu Glu Trp Ile
35 40 45

ggg tat atc tat tac agt ggg agc acc aac tac aac ccc tcc ctc aag 192
Gly Tyr Ile Tyr Tyr Ser Gly Ser Thr Asn Tyr Asn Pro Ser Leu Lys
50 55 60

agt cga gtc acc ata tca gta gac acg tcc aag aac cag ttc tcc ctg 240
Ser Arg Val Thr Ile Ser Val Asp Thr Ser Lys Asn Gln Phe Ser Leu
65 70 75 80

aag ctg agc tct gtg acc gct gcg gac acg gcc gtg tat tac tgt gcg 288
Lys Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr Cys Ala
85 90 95

aga gat gtc atg cag cag ccg gta cgg ggt tac tac tac tac tac ggt 336
Arg Asp Val Met Gln Gln Pro Val Arg Gly Tyr Tyr Tyr Tyr Tyr Gly
100 105 110

atg gac gtc tgg ggc caa gga acc ctg gtc acc gtc tcc tca 378
Met Asp Val Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
115 120 125

<210> 68
<211> 126
<212> PRT
<213> Homo sapiens

<400> 68
Glu Val Gln Leu Val Glu Ser Gly Pro Gly Leu Val Lys Pro Ser Glu
1 5 10 15

Thr Leu Ser Leu Thr Cys Thr Val Ser Gly Gly Ser Ile Ser Ser Tyr
20 25 30

Tyr Trp Ser Trp Ile Arg Gln Pro Pro Gly Lys Gly Leu Glu Trp Ile
35 40 45

Gly Tyr Ile Tyr Tyr Ser Gly Ser Thr Asn Tyr Asn Pro Ser Leu Lys
50 55 60

Ser Arg Val Thr Ile Ser Val Asp Thr Ser Lys Asn Gln Phe Ser Leu
65 70 75 80

Lys Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr Cys Ala
85 90 95

Arg Asp Val Met Gln Gln Pro Val Arg Gly Tyr Tyr Tyr Tyr Tyr Gly
100 105 110

Met Asp Val Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
115 120 125

<210> 69
<211> 327
<212> DNA
<213> Homo sapiens

<220>
<221> CDS

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gaa att gtg ttg acg cag tct cca ggc acc ctg tct ttg tct cca ggg 48
Glu Ile Val Leu Thr Gln Ser Pro Gly Thr Leu Ser Leu Ser Pro Gly
1 5 10 15

gaa aga gtc acc ctc tcc tgc agg gcc agt cag aga gtt agc aac agc 96
Glu Arg Val Thr Leu Ser Cys Arg Ala Ser Gln Arg Val Ser Asn Ser
20 25 30

tac tta gcc tgg tac cag cag aaa cct ggc cag gct ccc agg ttc ctc 144
 Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Phe Leu
 35 40 45

atc tat ggt gta tcc agc agg gcc act ggc atc cca gac agg ttc agt 192
Ile Tyr Gly Val Ser Ser Arg Ala Thr Gly Ile Pro Asp Arg Phe Ser
50 55 60

ggc agt ggg tct ggg aca gac ttc act ctc acc atc agc aga ctg gag 240
Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Arg Leu Glu
65 70 75 80

cct gaa gat ttt gca gtg tat tac tgt cag cag tat ggt agt tca ccg 288
Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Tyr Gly Ser Ser Pro
85 90 95

tgg acg ttc ggc caa ggg acc aag gtg gaa atc aaa cga 327
Trp Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg
100 105

<211> 109

<212> PRT

<213> Homo sapiens

Glu Ile Val Leu Thr Gln Ser Pro Gly Thr Leu Ser Leu Ser Pro Gly
1 5 10 15

Glu Arg Val Thr Leu Ser Cys Arg Ala Ser Gln Arg Val Ser Asn Ser
20 25 30

Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Phe Leu
35 40 45

Ile Tyr Gly Val Ser Ser Arg Ala Thr Gly Ile Pro Asp Arg Phe Ser
50 55 60

Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Arg Leu Glu
65 70 75 80

Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Tyr Gly Ser Ser Pro
85 90 95

Trp Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg
100 105